

M. Pak.

RECEIVED Page 1 of 7
JUN 21 2001 #11 B
TECH CENTER 1600/2900 6/22/01
1646

RAW SEQUENCE LISTING DATE: 05/17/2001
PATENT APPLICATION: US/09/312,596A TIME: 10:10:14

Input Set : A:\593601.app
Output Set: N:\CRF3\05172001\I312596A.raw

3 <110> APPLICANT: Role, Lorna W.
4 Talmage, David
5 Bao, Jianxin
7 <120> TITLE OF INVENTION: A-FORM OF CYTOPLASMIC DOMAIN OF nARIA (CRD-NEUREGULIN
8 AND USES THEREOF
10 <130> FILE REFERENCE: 0575/59360
12 <140> CURRENT APPLICATION NUMBER: 09/312,596A
13 <141> CURRENT FILING DATE: 1999-05-14
15 <160> NUMBER OF SEQ ID NOS: 4
17 <170> SOFTWARE: PatentIn Ver. 2.1
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 3212
21 <212> TYPE: DNA
22 <213> ORGANISM: CHICKEN nARIA
24 <400> SEQUENCE: 1

ENTERED
see p.5

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27 aaggtgagag tcttgccctt cgctctgggc tattggttca cttaatccgg tcaatttggt 180
28 cgctgctcgt ggttgctctt ctcgccgcc ccttccccc tgttttggtt tgtttcgctt 240
29 gctttcgggg ggacgctcct tccctcagtc agaagagctg gaattgcttg agaggcgtat 300
30 aaggaattat aaaagtggcc aggaacacg agcgcagtga ctgcagagct gcccttggct 360
31 tcggcaaggc agcgtgagcg gcagagggct cgggcaagg ggggggggct cctttttcc 420
32 cgtgctgtcc tcttctccca gttcggatga tgttgctgtt tcggacctct cgctgactcc 480
33 tgccctgtga tttttgtga gcgctgtgac tgttactcog tctctttctg tctgtgtttc 540
34 acagtaattg actgtgatag agttaaggcc ttttgagggt gagctgtgtc acagctgatg 600
35 cttaaacatg tctgaagtag gcaccgagac tttccccagc cctcgggctc agctgagccc 660
36 tgatgcatcc cttggcgggc tcccggctga ggagaacatg ccggggcccc acagagagga 720
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40 gtatgactct cctacacacc ttgacctgg gaggatagga caagacccaa ggagcactgt 960
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47 ctacatggta aaagacctcc caaacctcc acgataccta tgcagggtgcc caaatgaatt 1380
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53 gtacgtttca aaaaacataa tctccagtga acgtgtcgtt gagcgagaaa ccgagacctc 1740
54 gttttccaca agccactaca cctcaacaac tcatcactcc atgacagtca ccagacgcc 1800
55 tagccacagc tggagtaatg gccataccga aagcattctc tccgaaagcc actccgtgct 1860
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57 caatggcatt ggtgggccaa ggaaggcaa cagcttcctc cggcatgcaa gagagacccc 1980
58 tgactcctac cgagactctc ctcacagtga aaggtatgtc tcagctatga ccacaccagc 2040
59 tcgcatgtca cccgttgatt tccacactcc aacttctccc aagtcccctc catctgaaat 2100
60 gtcaccacca gtttcagct tgaccatctc catcccttcg gtggcgtgga gtccctttat 2160
61 ggacgaggag agaccgctgc tgttggtgac cccaccacgg ctgctgaga agtacgacaa 2220
62 ccaccttcag caattcaact ccttocacaa caatccacc catgagagca acagtctgcc 2280
63 acccagtcct ctgaggatag tggaggatga agagtatgag accacgcagg agtacgaacc 2340
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65 tggccatatt tccagcaggg tagaagtgga ctccgacaca agctctcaga gcactagctc 2460
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67 tcccatggca accagtctgg agccagccgc tgcatatcgg ctggctgaga acaggactaa 2580
68 cccggcaaat cgcttctcca caccagaaga gttgcaagca aggttgtcca gtgtaatagc 2640
69 taaccaagac cctattgctg tataagacat aaacaaaaca catagattca catgtaaaac 2700
70 tttattttat ataatgaagt attccacctt taaattaaac aatttatttt attttagcaa 2760
71 ttccgctgat agaaaacaag agtggaaaaa gaaactttta taaattaagt atacgtatgt 2820
72 acaaatgtgt tatgtgccat atgtagcaat tttttacagt atttccaaa tggggaaaga 2880
73 tatcaatggt gcctttatgt tatgttatgt tgagagcaag tttgtacag ctacaatgat 2940
74 tgctgtcccg tagtattttg caaaaccttc tagccctcag ttgttctggc tttttgtgc 3000
75 attgcattat aatgactgga tgtatgattt gcaagaattg cagaagtccc catttgcttg 3060
76 ttgtggaatc cccagatcaa aaagccctgt tatggcactc acaccctatc cacttcacca 3120
77 ggaaaaaaaa aaatcaaaa aaaaaaaaaa aaaaaaaga aaagaaagag aaaaaagaaa 3180
78 agaaaaagaa aaaaaaagct gaaaaaataa aa 3212

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81 <210> SEQ ID NO: 2

82 <211> LENGTH: 1070

83 <212> TYPE: PRT

84 <213> ORGANISM: CHICKEN nARIA

86 <220> FEATURE:

87 <221> NAME/KEY: UNSURE

88 <222> LOCATION: (32)

89 <223> OTHER INFORMATION: Wherein Xaa = unclear results

91 <220> FEATURE:

92 <221> NAME/KEY: UNSURE

93 <222> LOCATION: (42)

94 <223> OTHER INFORMATION: Wherein Xaa = unclear results

96 <220> FEATURE:

97 <221> NAME/KEY: UNSURE

98 <222> LOCATION: (113)

99 <223> OTHER INFORMATION: Wherein Xaa = unclear results

101 <220> FEATURE:

102 <221> NAME/KEY: UNSURE

103 <222> LOCATION: (163)

104 <223> OTHER INFORMATION: Wherein Xaa = unclear results

106 <220> FEATURE:

107 <221> NAME/KEY: UNSURE

108 <222> LOCATION: (182)

109 <223> OTHER INFORMATION: Wherein Xaa = unclear results

111 <220> FEATURE:

112 <221> NAME/KEY: UNSURE

113 <222> LOCATION: (199)

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114 <223> OTHER INFORMATION: Wherein Xaa = unclear results
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117 <221> NAME/KEY: UNSURE
118 <222> LOCATION: (888)
119 <223> OTHER INFORMATION: Wherein Xaa = unclear results
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122 <221> NAME/KEY: UNSURE
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124 <223> OTHER INFORMATION: Wherein Xaa = unclear results
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128 <222> LOCATION: (984)
129 <223> OTHER INFORMATION: Wherein Xaa = unclear results
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132 <221> NAME/KEY: UNSURE
133 <222> LOCATION: (1067)
134 <223> OTHER INFORMATION: Wherein Xaa = unclear results
136 <400> SEQUENCE: 2
137 Gly Cys Cys Cys Tyr Cys His Phe Cys Arg Cys Arg Cys Cys Tyr Arg
138   1           5           10           15
W--> 140 Phe Cys Phe Cys Ser Phe Tyr Arg Met Thr Ile Val Phe Leu Ala Xaa
141           20           25           30
W--> 143 Ala Asp Thr Ser Leu Arg Cys Ser Arg Xaa Glu Ser Cys Leu Ser Leu
144           35           40           45
146 Trp Ala Ile Gly Ser Leu Asn Pro Val Asn Leu Phe Ala Ala Arg Gly
147   50           55           60
149 Cys Leu Ser Pro Arg Pro Ser Pro Cys Phe Val Leu Phe Arg Leu
150  65           70           75           80
152 Leu Ser Gly Gly Arg Ser Phe Pro Gln Ser Glu Glu Leu Glu Leu Leu
153           85           90           95
155 Glu Arg Arg Ile Arg Asn Tyr Lys Ser Gly Gln Glu Thr Arg Ala Gln
156   /           100          105          110
W--> 158 Xaa Leu Gln Ser Cys Pro Trp Leu Arg Gln Gly Ser Val Ser Gly Arg
159           115           120           125
161 Gly Leu Gly Gln Gly Ala Gly Gly Leu Leu Phe Pro Val Arg Ser Ser
162   130           135           140
164 Ser Pro Ser Ser Asp Asp Val Ala Val Ser Asp Leu Ser Leu Thr Pro
165 145 /           150           155           160
W--> 167 Ala Leu Xaa Phe Leu Leu Ser Ala Val Thr Val Thr Pro Ser Leu Ser
168           165           170           175
W--> 170 Val Cys Val Ser Gln Xaa Trp Thr Val Ile Glu Leu Arg Pro Phe Gly
171           180           185           190
W--> 173 Gly Glu Leu Cys His Ser Xaa Cys Leu Asn Met Ser Glu Val Gly Thr
174           195           200           205
176 Glu Thr Phe Pro Ser Pro Ser Ala Gln Leu Ser Pro Asp Ala Ser Leu
177   210           215           220
179 Gly Gly Leu Pro Ala Glu Glu Asn Met Pro Gly Pro His Arg Glu Asp
180 225           230           235           240
182 Ser Arg Val Pro Gly Val Ala Gly Leu Ala Ser Thr Cys Cys Val Cys

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183		245		250		255
185	Leu Glu Ala Glu Arg Leu Lys Gly Cys Leu Asn Ser Glu Lys Ile Cys					
186		260		265		270
188	Ile Ala Pro Ile Leu Ala Cys Leu Leu Ser Leu Cys Leu Cys Ile Ala					
189		275		280		285
191	Gly Leu Lys Trp Val Phe Val Asp Lys Ile Phe Glu Tyr Asp Ser Pro					
192		290		295		300
194	Thr His Leu Asp Pro Gly Arg Ile Gly Gln Asp Pro Arg Ser Thr Val					
195	305		310		315	320
197	Asp Pro Thr Ala Leu Ser Ala Trp Val Pro Ser Glu Val Tyr Ala Ser					
198		325		330		335
200	Pro Phe Pro Ile Pro Ser Leu Glu Ser Lys Ala Glu Val Thr Val Gln					
201		340		345		350
203	Thr Asp Ser Ser Leu Val Pro Ser Arg Pro Phe Leu Gln Pro Ser Leu					
204		355		360		365
206	Tyr Asn Arg Ile Leu Asp Val Gly Leu Trp Ser Ser Ala Thr Pro Ser					
207		370		375		380
209	Leu Ser Pro Ser Ser Leu Glu Pro Thr Thr Ala Ser Gln Ala Gln Ala					
210	385		390		395	400
212	Thr Glu Thr Asn Leu Gln Thr Ala Pro Lys Leu Ser Thr Ser Thr Ser					
213		405		410		415
215	Thr Thr Gly Thr Ser His Leu Thr Lys Cys Asp Ile Lys Gln Lys Ala					
216		420		425		430
218	Phe Cys Val Asn Gly Gly Glu Cys Tyr Met Val Lys Asp Leu Pro Asn					
219		435		440		445
221	Pro Pro Arg Tyr Leu Cys Arg Cys Pro Asn Glu Phe Thr Gly Asp Arg					
222		450		455		460
224	Cys Gln Asn Tyr Val Met Ala Ser Phe Tyr Lys His Leu Gly Ile Glu					
225	465		470		475	480
227	Phe Met Glu Ala Glu Glu Leu Tyr Gln Lys Arg Val Leu Thr Ile Thr					
228		485		490		495
230	Gly Ile Cys Ile Ala Leu Leu Val Val Gly Ile Met Cys Val Val Ala					
231		500		505		510
233	Tyr Cys Lys Thr Lys Lys Gln Arg Lys Lys Leu His Asp Arg Leu Arg					
234		515		520		525
236	Gln Ser Leu Arg Ser Glu Arg Asn Asn Val Met Asn Met Ala Asn Gln					
237		530		535		540
239	Pro His His Pro Asn Pro Pro Asp Asn Val Gln Leu Val Asn Gln					
240	545		550		555	560
242	Tyr Val Ser Lys Asn Ile Ile Ser Ser Glu Arg Val Val Glu Arg Glu					
243		565		570		575
245	Thr Glu Thr Ser Phe Ser Thr Ser His Tyr Thr Ser Thr Thr His His					
246		580		585		590
248	Ser Met Thr Val Thr Gln Thr Pro Ser His Ser Trp Ser Asn Gly His					
249		595		600		605
251	Thr Glu Ser Ile Leu Ser Glu Ser His Ser Val Leu Val Ser Ser Ser					
252		610		615		620
254	Val Glu Asn Ser Arg His Thr Ser Pro Thr Gly Pro Arg Gly Arg Leu					
255	625		630		635	640

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257 Asn Gly Ile Gly Gly Pro Arg Glu Gly Asn Ser Phe Leu Arg His Ala
258                               645                               650                               655
260 Arg Glu Thr Pro Asp Ser Tyr Arg Asp Ser Pro His Ser Glu Arg Tyr
261                               660                               665                               670
263 Val Ser Ala Met Thr Thr Pro Ala Arg Met Ser Pro Val Asp Phe His
264                               675                               680                               685
266 Thr Pro Thr Ser Pro Lys Ser Pro Pro Ser Glu Met Ser Pro Pro Val
267                               690                               695                               700
269 Ser Ser Leu Thr Ile Ser Ile Pro Ser Val Ala Val Ser Pro Phe Met
270 705                               710                               715                               720
272 Asp Glu Glu Arg Pro Leu Leu Leu Val Thr Pro Pro Arg Leu Arg Glu
273                               725                               730                               735
275 Lys Tyr Asp Asn His Leu Gln Gln Phe Asn Ser Phe His Asn Asn Pro
276                               740                               745                               750
278 Thr His Glu Ser Asn Ser Leu Pro Pro Ser Pro Leu Arg Ile Val Glu
279                               755                               760                               765
281 Asp Glu Glu Tyr Glu Thr Thr Gln Glu Tyr Glu Pro Ala Gln Glu Pro
282                               770                               775                               780
284 Pro Lys Lys Leu Thr Asn Ser Arg Arg Val Lys Arg Thr Lys Pro Asn
285 785                               790                               795                               800
287 Gly His Ile Ser Ser Arg Val Glu Val Asp Ser Asp Thr Ser Ser Gln
288                               805                               810                               815
290 Ser Thr Ser Ser Glu Ser Glu Thr Glu Asp Glu Arg Ile Gly Glu Asp
291                               820                               825                               830
293 Thr Pro Phe Leu Ser Ile Gln Asn Pro Met Ala Thr Ser Leu Glu Pro
294                               835                               840                               845
296 Ala Ala Ala Tyr Arg Leu Ala Glu Asn Arg Thr Asn Pro Ala Asn Arg
297                               850                               855                               860
299 Phe Ser Thr Pro Glu Glu Leu Gln Ala Arg Leu Ser Ser Val Ile Ala
300 865                               870                               875                               880
W--> 302 Asn Gln Asp Pro Ile Ala Val Xaa Asp Ile Asn Lys Thr His Arg Phe
303                               885                               890                               895
305 Thr Cys Lys Thr Leu Phe Tyr Ile Met Lys Tyr Ser Thr Phe Lys Leu
306                               900                               905                               910
308 Asn Asn Leu Phe Tyr Phe Ser Asn Ser Ala Asp Arg Lys Gln Glu Trp
309                               915                               920                               925
W--> 311 Lys Lys Lys Leu Leu Xaa Ile Lys Tyr Thr Tyr Val Gln Met Cys Tyr
312                               930                               935                               940
314 Val Pro Tyr Val Ala Ile Phe Tyr Ser Ile Ser Lys Met Gly Lys Asp
315 945                               950                               955                               960
317 Ile Asn Gly Ala Phe Met Leu Cys Tyr Val Glu Ser Lys Phe Cys Thr
318                               965                               970                               975
W--> 320 Ala Thr Met Ile Ala Val Pro Xaa Tyr Phe Ala Lys Pro Ser Ser Pro
321                               980                               985                               990
323 Gln Leu Phe Trp Leu Phe Cys Ala Leu His Tyr Asn Asp Trp Met Tyr
324                               995                               1000                               1005
326 Asp Leu Gln Glu Leu Gln Lys Ser Pro Phe Ala Cys Cys Gly Ile Pro
327 1010                               1015                               1020
329 Arg Ser Lys Ser Pro Val Met Ala Leu Thr Pro Tyr Pro Leu His Gln

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

DATE: 05/17/2001

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Input Set : A:\593601.app

Output Set: N:\CRF3\05172001\I312596A.raw

L:140 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:143 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:158 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:167 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:170 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:173 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:302 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:311 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:320 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:335 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:426 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:489 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:492 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:495 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:498 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:501 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:504 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:507 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4